

Serial Number: 09/830,446

CRF Processing Date: 11/7/01  
 Edited by: JC  
 Verified by:            (STIC sta

ENTERED

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line
- ☐ Edited a format error in the Current Application Data section, specifically: \_\_\_\_\_
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other \_\_\_\_\_
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: \_\_\_\_\_
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: \_\_\_\_\_
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: \_\_\_\_\_
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: \_\_\_\_\_
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: \_\_\_\_\_
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as \_\_\_\_\_
- ☐ Inserted mandatory headings, specifically: \_\_\_\_\_
- ☒ Corrected an obvious error in the response, specifically:  
Seq. Nos. 36 + 45 - Misnumbering of codons; were properly corrected
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: \_\_\_\_\_
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: \_\_\_\_\_
- ☐ Other: \_\_\_\_\_

\*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

PCT09

## RAW SEQUENCE LISTING

DATE: 11/07/2001

PATENT APPLICATION: US/09/830,446

TIME: 12:36:47

Input Set : A:\PTO.DC.txt

Output Set: N:\CRF3\11072001\I830446.raw

3 <110> APPLICANT: MURDIN, Andrew D.; OOMEN, Raymond P; and WANG, Joe  
 5 <120> TITLE OF INVENTION: Chlamydia antigens and corresponding DNA fragments and uses  
 thereof

7 <130> FILE REFERENCE: 77813-51  
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/830,446  
 C--> 10 <141> CURRENT FILING DATE: 2001-09-21  
 12 <150> PRIOR APPLICATION NUMBER: US 60/106034  
 13 <151> PRIOR FILING DATE: 1998-10-28  
 14 <150> PRIOR APPLICATION NUMBER: US 60/106039  
 15 <151> PRIOR FILING DATE: 1998-10-28  
 16 <150> PRIOR APPLICATION NUMBER: US 60/10604  
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 19 <151> PRIOR FILING DATE: 1998-10-28  
 20 <150> PRIOR APPLICATION NUMBER: US 60/106072  
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 24 <150> PRIOR APPLICATION NUMBER: US 60/106074  
 25 <151> PRIOR FILING DATE: 1998-10-29  
 26 <150> PRIOR APPLICATION NUMBER: US 60/106087  
 27 <151> PRIOR FILING DATE: 1998-10-29  
 28 <150> PRIOR APPLICATION NUMBER: US 60/106587  
 29 <151> PRIOR FILING DATE: 1998-11-02  
 30 <150> PRIOR APPLICATION NUMBER: US 60/106588  
 31 <151> PRIOR FILING DATE: 1998-11-02  
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 35 <151> PRIOR FILING DATE: 1998-11-02  
 36 <150> PRIOR APPLICATION NUMBER: US 60/107035  
 37 <151> PRIOR FILING DATE: 1998-11-02  
 39 <160> NUMBER OF SEQ ID NOS: 45  
 41 <170> SOFTWARE: PatentIn Ver. 2.0  
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 44 <211> LENGTH: 2750  
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 56 Met Lys Ile Pro Leu  
 57 1 5  
 59 cgc ttt tta ttg ata tca tta gta cct acg ctt tct atg tcg aat tta 163  
 60 Arg Phe Leu Leu Ile Ser Leu Val Pro Thr Leu Ser Met Ser Asn Leu

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64	Leu Gly Ala Ala Thr Thr Glu Glu Leu Ser Ala Ser Asn Ser Phe Asp						
65		25		30		35	
67	gga act aca tca aca aca agc ttt tct agt aaa aca tca tcg gct aca						259
68	Gly Thr Thr Ser Thr Thr Ser Phe Ser Ser Lys Thr Ser Ser Ala Thr						
69		40		45		50	
71	gat ggc acc aat tat gtt ttt aaa gat tct gta gtt ata gaa aat gta						307
72	Asp Gly Thr Asn Tyr Val Phe Lys Asp Ser Val Val Ile Glu Asn Val						
73		55		60		65	
75	ccc aaa aca ggg gaa act cag tct act agt tgt ttt aaa aat gac gct						355
76	Pro Lys Thr Gly Glu Thr Gln Ser Thr Ser Cys Phe Lys Asn Asp Ala						
77	70		75		80		85
79	gca gct gga gat cta aat ttc tta gga ggg gga ttt tct ttc aca ttt						403
80	Ala Ala Gly Asp Leu Asn Phe Leu Gly Gly Gly Phe Ser Phe Thr Phe						
81		90		95		100	
83	agc aat atc gat gca acc acg gct tct gga gct gct att gga agt gaa						451
84	Ser Asn Ile Asp Ala Thr Thr Ala Ser Gly Ala Ala Ile Gly Ser Glu						
85		105		110		115	
87	gca gct aat aag aca gtc acg tta tca gga ttt tcg gca ctt tct ttt						499
88	Ala Ala Asn Lys Thr Val Thr Leu Ser Gly Phe Ser Ala Leu Ser Phe						
89		120		125		130	
91	ctt aaa tcc cca gca agt aca gtg act aat gga ttg gga gct atc aat						547
92	Leu Lys Ser Pro Ala Ser Thr Val Thr Asn Gly Leu Gly Ala Ile Asn						
93		135		140		145	
95	gtt aaa ggg aat tta agc cta ttg gat aat gat aag gta ttg att cag						595
96	Val Lys Gly Asn Leu Ser Leu Leu Asp Asn Asp Lys Val Leu Ile Gln						
97	150		155		160		165
99	gac aat ttc tca aca gga gat ggc gga gca att aat tgt gca ggc tcc						643
100	Asp Asn Phe Ser Thr Gly Asp Gly Gly Ala Ile Asn Cys Ala Gly Ser						
101		170		175		180	
103	ttg aag atc gca aac aat aag tcc ctt tct ttt att gga aat agt tct						691
104	Leu Lys Ile Ala Asn Asn Lys Ser Leu Ser Phe Ile Gly Asn Ser Ser						
105		185		190		195	
107	tca aca cgt ggc gga gcg att cat acc aaa aac ctc aca cta tct tct						739
108	Ser Thr Arg Gly Gly Ala Ile His Thr Lys Asn Leu Thr Leu Ser Ser						
109		200		205		210	
111	ggt ggg gaa act cta ttt cag ggg aat aca gcg cct acg gct gct ggt						787
112	Gly Gly Glu Thr Leu Phe Gln Gly Asn Thr Ala Pro Thr Ala Ala Gly						
113		215		220		225	
115	aaa gga ggt gct atc gcg att gca gac tct ggc acc cta tcc att tct						835
116	Lys Gly Gly Ala Ile Ala Ile Ala Asp Ser Gly Thr Leu Ser Ile Ser						
117	230		235		240		245
119	gga gac agt ggc gac att atc ttt gaa ggc aat acg ata gga gct aca						883
120	Gly Asp Ser Gly Asp Ile Ile Phe Glu Gly Asn Thr Ile Gly Ala Thr						
121		250		255		260	
123	gga acc gtc tct cat agt gct att gat tta gga act agc gct aag ata						931
124	Gly Thr Val Ser His Ser Ala Ile Asp Leu Gly Thr Ser Ala Lys Ile						
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131 att act gta aca gga tcg aca tct gtt gct gat gct ctc aat att aat 1027
132 Ile Thr Val Thr Gly Ser Thr Ser Val Ala Asp Ala Leu Asn Ile Asn
133      295      300      305
135 agc cct gat act gga gat aac aaa gag tat acg gga acc ata gtc ttt 1075
136 Ser Pro Asp Thr Gly Asp Asn Lys Glu Tyr Thr Gly Thr Ile Val Phe
137 310      315      320      325
139 tct gga gag aag ctc acg gag gca gaa gct aaa gat gag aag aac cgc 1123
140 Ser Gly Glu Lys Leu Thr Glu Ala Glu Ala Lys Asp Glu Lys Asn Arg
141      330      335      340
143 act tct aaa tta ctt caa aat gtt gct ttt aaa aat ggg act gta gtt 1171
144 Thr Ser Lys Leu Leu Gln Asn Val Ala Phe Lys Asn Gly Thr Val Val
145      345      350      355
147 tta aaa ggt gat gtc gtt tta agt gcg aac ggt ttc tct cag gat gca 1219
148 Leu Lys Gly Asp Val Val Leu Ser Ala Asn Gly Phe Ser Gln Asp Ala
149      360      365      370
151 aac tct aag ttg att atg gat tta ggg acg tcg ttg gtt gca aac acc 1267
152 Asn Ser Lys Leu Ile Met Asp Leu Gly Thr Ser Leu Val Ala Asn Thr
153      375      380      385
155 gaa agt atc gag tta acg aat ttg gaa att aat ata gac tct ctc agg 1315
156 Glu Ser Ile Glu Leu Thr Asn Leu Glu Ile Asn Ile Asp Ser Leu Arg
157 390      395      400      405
159 aac ggg aaa aag ata aaa ctc agt gct gcc aca gct cag aaa gat att 1363
160 Asn Gly Lys Lys Ile Lys Leu Ser Ala Ala Thr Ala Gln Lys Asp Ile
161      410      415      420
163 cgt ata gat cgt cct gtt gta ctg gca att agc gat gag agt ttt tat 1411
164 Arg Ile Asp Arg Pro Val Val Leu Ala Ile Ser Asp Glu Ser Phe Tyr
165      425      430      435
167 caa aat ggc ttt ttg aat gag gac cat tcc tat gat ggg att ctt gag 1459
168 Gln Asn Gly Phe Leu Asn Glu Asp His Ser Tyr Asp Gly Ile Leu Glu
169      440      445      450
171 tta gat gct ggg aaa gac atc gtg att tct gca gat tct cgc agt ata 1507
172 Leu Asp Ala Gly Lys Asp Ile Val Ile Ser Ala Asp Ser Arg Ser Ile
173      455      460      465
175 gat gct gta caa tct ccg tat ggc tat cag gga aag tgg acg atc aat 1555
176 Asp Ala Val Gln Ser Pro Tyr Gly Tyr Gln Gly Lys Trp Thr Ile Asn
177 470      475      480      485
179 tgg tct act gat gat aag aaa gct acg gtt tct tgg gcg aag cag agt 1603
180 Trp Ser Thr Asp Asp Lys Lys Ala Thr Val Ser Trp Ala Lys Gln Ser
181      490      495      500
183 ttt aat ccc act gct gag cag gag gct ccg tta gtt cct aat ctt ctt 1651
184 Phe Asn Pro Thr Ala Glu Gln Glu Ala Pro Leu Val Pro Asn Leu Leu
185      505      510      515
187 tgg ggt tct ttt ata gat gtt cgt tcc ttc cag aat ttt ata gag cta 1699
188 Trp Gly Ser Phe Ile Asp Val Arg Ser Phe Gln Asn Phe Ile Glu Leu
189      520      525      530
191 ggt act gaa ggt gct cct tac gaa aag aga ttt tgg gtt gca ggc att 1747

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197 550      555      560      565
199 cat gtg agt gga ggt gct gta gta ggt gct agc acg agg atg ccg ggt 1843
200 His Val Ser Gly Gly Ala Val Val Gly Ala Ser Thr Arg Met Pro Gly
201      570      575      580
203 ggt gat acc ttg tct ctg ggt ttt gct cag ctg ttt gcg cgt gac aaa 1891
204 Gly Asp Thr Leu Ser Leu Gly Phe Ala Gln Leu Phe Ala Arg Asp Lys
205      585      590      595
207 gac tac ttt atg aat acc aat ttc gca aag acc tac gca gga tct tta 1939
208 Asp Tyr Phe Met Asn Thr Asn Phe Ala Lys Thr Tyr Ala Gly Ser Leu
209      600      605      610
211 cgt ttg cag cac gat gct tcc cta tac tct gtg gtg agt atc ctt tta 1987
212 Arg Leu Gln His Asp Ala Ser Leu Tyr Ser Val Val Ser Ile Leu Leu
213      615      620      625
215 gga gag gga gga ctg cgc gag atc ctg ttg cct tat gtt tcc aag act 2035
216 Gly Glu Gly Gly Leu Arg Glu Ile Leu Leu Pro Tyr Val Ser Lys Thr
217 630      635      640      645
219 ctg ccg tgc tct ttc tat ggg cag ctt agc tac ggc cat acg gat cat 2083
220 Leu Pro Cys Ser Phe Tyr Gly Gln Leu Ser Tyr Gly His Thr Asp His
221      650      655      660
223 cgc atg aag acc gag tct cta ccc ccc ccc ccc ccg acg ctg tcg acg 2131
224 Arg Met Lys Thr Glu Ser Leu Pro Pro Pro Pro Pro Thr Leu Ser Thr
225      665      670      675
227 gat cat act tct tgg gga gga tat gtc tgg gct gga gag ctg gga act 2179
228 Asp His Thr Ser Trp Gly Gly Tyr Val Trp Ala Gly Glu Leu Gly Thr
229      680      685      690
231 cga gtt gct gtt gaa aat acc agc ggc aga gga ttt ttc caa gag tac 2227
232 Arg Val Ala Val Glu Asn Thr Ser Gly Arg Gly Phe Phe Gln Glu Tyr
233      695      700      705
235 act cca ttt gta aaa gtc caa gct gtt tac gct cgc caa gat agc ttt 2275
236 Thr Pro Phe Val Lys Val Gln Ala Val Tyr Ala Arg Gln Asp Ser Phe
237 710      715      720      725
239 gta gaa cta gga gct atc agt cgt gat ttt agt gat tcg cat ctt tat 2323
240 Val Glu Leu Gly Ala Ile Ser Arg Asp Phe Ser Asp Ser His Leu Tyr
241      730      735      740
243 aac ctt gcg att cct ctt gga atc aag tta gag aaa cgg ttt gca gag 2371
244 Asn Leu Ala Ile Pro Leu Gly Ile Lys Leu Glu Lys Arg Phe Ala Glu
245      745      750      755
247 caa tat tat cat gtt gta gcg atg tat tct cca gat gtt tgt cgt agt 2419
248 Gln Tyr Tyr His Val Val Ala Met Tyr Ser Pro Asp Val Cys Arg Ser
249      760      765      770
251 aac ccc aaa tgt acg act acc cta ctt tcc aac caa ggg agt tgg aag 2467
252 Asn Pro Lys Cys Thr Thr Thr Leu Leu Ser Asn Gln Gly Ser Trp Lys
253      775      780      785
255 acc aaa ggt tcg aac tta gca aga cag gct ggt att gtt cag gcc tca 2515
256 Thr Lys Gly Ser Asn Leu Ala Arg Gln Ala Gly Ile Val Gln Ala Ser

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263 ttt gaa tgg cgg gga tct tct cgt agc tat aat gta gat gcg ggt agc 2611
264 Phe Glu Trp Arg Gly Ser Ser Arg Ser Tyr Asn Val Asp Ala Gly Ser
265          825          830          835
267 aaa atc aaa ttt tagcgatttc tctttcgatg ctattttttcc atggctatatt 2663
268 Lys Ile Lys Phe
269          840
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277 <211> LENGTH: 2523
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291          10          15          20
293 tta gga gct gct act acc gaa gag tta tcg gct agc aat agc ttc gat 111
294 Leu Gly Ala Ala Thr Thr Glu Glu Leu Ser Ala Ser Asn Ser Phe Asp
295          25          30          35
297 gga act aca tca aca aca agc ttt tct agt aaa aca tca tcg gct aca 159
298 Gly Thr Thr Ser Thr Thr Ser Phe Ser Ser Lys Thr Ser Ser Ala Thr
299          40          45          50
301 gat ggc acc aat tat gtt ttt aaa gat tct gta gtt ata gaa aat gta 207
302 Asp Gly Thr Asn Tyr Val Phe Lys Asp Ser Val Val Ile Glu Asn Val
303          55          60          65
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306 Pro Lys Thr Gly Glu Thr Gln Ser Thr Ser Cys Phe Lys Asn Asp Ala
307 70          75          80          85
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314 Ser Asn Ile Asp Ala Thr Thr Ala Ser Gly Ala Ala Ile Gly Ser Glu
315          105          110          115
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319          120          125          130
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322 Leu Lys Ser Pro Ala Ser Thr Val Thr Asn Gly Leu Gly Ala Ile Asn
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**VERIFICATION SUMMARY**

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DATE: 11/07/2001

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L:9 M:270 C: Current Application Number differs, Replaced Current Application Number

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date